

#2

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PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/067,477

DATE: 05/02/2002
TIME: 15:07:19

INPUT SET: S36844.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4 (1) GENERAL INFORMATION:
--> 5 (i) APPLICANT:
--> 6 (A) NAME: Shuji HINUMA
--> 7 (B) STREET: 7-9-1402, Kasuga 1-chome
--> 8 (C) CITY: Tsukuba
--> 9 (D) STATE: Ibaraki
--> 10 (E) COUNTRY: Japan
--> 11 (F) POSTAL CODE (ZIP): 305
12
13 APPLICANT:
--> 14 (A) NAME: Junichi SAKAMOTO
--> 15 (B) STREET: 14-30-A103, Kamishinden 1-chome
--> 16 (C) CITY: Toyonaka
--> 17 (D) STATE: Osaka
--> 18 (E) COUNTRY: Japan
--> 19 (F) POSTAL CODE (ZIP): 565
20
21 APPLICANT:
--> 22 (A) NAME: Masaki HOSOYA
--> 23 (B) STREET: 711-83, Itaya 1-chome
--> 24 (C) CITY: Tsuchiura
--> 25 (D) STATE: Ibaraki
--> 26 (E) COUNTRY: Japan
--> 27 (F) POSTAL CODE (ZIP): 300
28
29 (ii) TITLE OF INVENTION: G Protein Coupled Receptor Proteins,
30 Their Production And Use
31
32 (iii) NUMBER OF SEQUENCES: 19
33
34 (iv) CORRESPONDENCE ADDRESS:
35 (A) ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
36 (B) STREET: 130 Water Street
37 (C) CITY: Boston
38 (D) STATE: MA
39 (E) COUNTRY: USA
40 (F) ZIP: 02109
41
42 (v) COMPUTER READABLE FORM:
43 (A) MEDIUM TYPE: Diskette
44 (B) COMPUTER: IBM Compatible
45 (C) OPERATING SYSTEM: DOS
46 (D) SOFTWARE: FastSEQ Version 1.5

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/067,477DATE: 05/02/2002
TIME: 15:07:20

INPUT SET: S36844.raw

47
48 (vi) CURRENT APPLICATION DATA:
49 (A) APPLICATION NUMBER: 10/067,477
50 (B) FILING DATE:
51 (C) CLASSIFICATION
52
53 (vii) PRIOR APPLICATION DATA:
54
55 (A) APPLICATION NUMBER: 08/796,570
56 (B) FILING DATE: 06-FEB-1997
57
58
59 (A) APPLICATION NUMBER: Japan 8-021562
60 (B) FILING DATE: 2-JUL-1996
61
62 (viii) ATTORNEY/AGENT INFORMATION:
63 (A) NAME: Eisenstein, Ronald I.
64 (B) REGISTRATION NUMBER: 30,628
65 (C) REFERENCE/DOCKET NUMBER: 47147
66
67 (ix) TELECOMMUNICATION INFORMATION:
68 (A) TELEPHONE: 617-523-3400
69 (B) TELEFAX: 617-523-6440
70
71 (2) INFORMATION FOR SEQ ID NO:1:
72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 423
74 (B) TYPE: Amino acid
75 (C) TOPOLOGY: Linear
76 (ii) MOLECULE TYPE: Peptide
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
78
79 Met Val Pro His Leu Leu Leu Cys Leu Leu Pro Leu Val Arg Ala
80 1 5 10 15
81 Thr Glu Pro His Glu Gly Arg Ala Asp Glu Gln Ser Ala Glu Ala Ala
82 20 25 30
83 Leu Ala Val Pro Asn Ala Ser His Phe Phe Ser Trp Asn Asn Tyr Thr
84 35 40 45
85 Phe Ser Asp Trp Gln Asn Phe Val Gly Arg Arg Arg Tyr Gly Ala Glu
86 50 55 60
87 Ser Gln Asn Pro Thr Val Lys Ala Leu Leu Ile Val Ala Tyr Ser Phe
88 65 70 75 80
89 Ile Ile Val Phe Ser Leu Phe Gly Asn Val Leu Val Cys His Val Ile
90 85 90 95
91 Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser Leu Phe Ile Val Asn
92 100 105 110
93 Leu Ala Val Ala Asp Ile Met Ile Thr Leu Leu Asn Thr Pro Phe Thr
94 115 120 125
95 Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe Gly Lys Gly Met Cys
96 130 135 140
97 His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu His Val Ser Ala Leu
98 145 150 155 160
99 Thr Leu Thr Ala Ile Ala Val Asp Arg His Gln Val Ile Met His Pro

RAW SEQUENCE LISTING PATENT APPLICATION US/10/067,477

DATE: 05/02/2002
TIME: 15:07:20

INPUT SET: S36844.raw

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100 165 170 175
101 Leu Lys Pro Arg Ile Ser Ile Thr Lys Gly Val Ile Tyr Ile Ala Val
102 180 185 190
103 Ile Trp Thr Met Ala Thr Phe Phe Ser Leu Pro His Ala Ile Cys Gln
104 195 200 205
105 Lys Leu Phe Thr Phe Lys Tyr Ser Glu Asp Ile Val Arg Ser Leu Cys
106 210 215 220
107 Leu Pro Asp Phe Pro Glu Pro Ala Asp Leu Phe Trp Lys Tyr Leu Asp
108 225 230 235 240
109 Leu Ala Thr Phe Ile Leu Leu Tyr Ile Leu Pro Leu Leu Ile Ile Ser
110 245 250 255
111 Val Ala Tyr Ala Arg Val Ala Lys Lys Leu Trp Leu Cys Asn Met Ile
112 260 265 270
113 Gly Asp Val Thr Thr Glu Gln Tyr Phe Ala Leu Arg Arg Lys Lys Lys
114 275 280 285
115 Lys Thr Ile Lys Met Leu Met Leu Val Val Val Leu Phe Ala Leu Cys
116 290 295 300
117 Trp Phe Pro Leu Asn Cys Tyr Val Leu Leu Leu Ser Ser Lys Val Ile
118 305 310 315 320
119 Arg Thr Asn Asn Ala Leu Tyr Phe Ala Phe His Trp Phe Ala Met Ser
120 325 330 335
121 Ser Thr Cys Tyr Asn Pro Phe Ile Tyr Cys Trp Leu Asn Glu Asn Phe
122 340 345 350
123 Arg Ile Glu Leu Lys Ala Leu Leu Ser Met Cys Gln Arg Pro Pro Lys
124 355 360 365
125 Pro Gln Glu Asp Arg Pro Pro Ser Pro Val Pro Ser Phe Arg Val Ala
126 370 375 380
127 Trp Thr Glu Lys Asn Asp Gly Gln Arg Ala Pro Leu Ala Asn Asn Leu
128 385 390 395 400
129 Leu Pro Thr Ser Gln Leu Gln Ser Gly Lys Thr Asp Leu Ser Ser Val
130 405 410 415
131 Glu Pro Ile Val Thr Met Ser
132 420
133

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

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136 (A) LENGTH: 1272
137 (B) TYPE: Nucleic acid
138 (C) STRANDEDNESS: Double
139 (C) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: cDNA

(xi) FEATURE:

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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144
145 ATGGTCCCTC ACCTCTTGCT GCTCTGTCTC CTCCCCTTGG TCGAGCCAC CGAGCCCCAC 60
146 GAGGGCCGGG CCGACGAGCA GAGCGCGGAG GCGGCCCTGG CCGTGCCCAA TGCCTCGCAC 120
147 TTCTTCTCTT GGAACAAC TA CACCTTCTCC GACTGGCAGA ACTTTGTGGG CAGGAGGCGC 180
148 TACGGCGCTG AGTCCCAGAA CCCCACGGTG AAAGCCCTGC TCATTGTGGC TTACTCCTTC 240
149 ATCATTGTCT TCTCACTCTT TGGCAACGTC CTGGTCTGTC ATGTCATCTT CAAGAACCAG 300
150 CGAATGCACT CGGCCACCAG CCTCTTCATC GTCAACCTGG CAGTTGCCGA CATAATGATC 360
151 ACGTGCTCA ACACCCCTT CACTTTGGTT CGCTTTGTGA ACAGCACATG GATATTTGGG 420
152 AAGGGCATGT GCCATGTCAG CCGCTTTGCC CAGTACTGCT CACTGCACGT CTCAGCACTG 480

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RAW SEQUENCE LISTING PATENT APPLICATION US/10/067,477

DATE: 05/02/2002
TIME: 15:07:20

INPUT SET: S36844.raw

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153 ACACTGACAG CCATTGCGGT GGATCGCCAC CAGGTCATCA TGCACCCCTT GAAACCCCGG 540
154 ATCTCAATCA CAAAGGGTGT CATCTACATC GCTGTCATCT GGACCATGGC TACGTTCTTT 600
155 TCACTCCAC ATGCTATCTG CCAGAAATTA TTTACCTTCA AATACAGTGA GGACATTGTG 660
156 CGCTCCCTCT GCCTGCCAGA CTTCCCTGAG CCAGCTGACC TCTTCTGGAA GTACCTGGAC 720
157 TTGGCCACCT TCATCCTGCT CTACATCCTG CCCCTCCTCA TCATCTCTGT GGCCTACGCT 780
158 CGTGTGGCCA AGAAACTGTG GCTGTGTAAT ATGATTGGCG ATGTGACCAC AGAGCAGTAC 840
159 TTTGCCCTGC GGCACAAAAA GAAGAAGACC ATCAAGATGT TGATGCTGGT GGTAGTCCTC 900
160 TTTGCCCTCT GCTGGTTCCC CCTCAACTGC TACGTCCTCC TCCTGTCCAG CAAGGTCATC 960
161 CGCACCAACA ATGCCCTCTA CTTTGCTTTC CACTGGTTTG CCATGAGCAG CACCTGCTAT 1020
162 AACCCCTTCA TATACTGCTG GCTGAACGAG AACTTCAGGA TTGAGCTAAA GGCAATTACTG 1080
163 AGCATGTGTC AAAGACCTCC CAAGCCTCAG GAGGACAGGC CACCCTCCCC AGTTCCTTCC 1140
164 TTCAGGGTGG CCTGGACAGA GAAGATGAT GGCCAGAGGG CTCCCCTTGC CAATAACCTC 1200
165 CTGCCCACCT CCAACTCCA GTCTGGGAAG ACAGACCTGT CATCTGTGGA ACCCATTTGTG 1260
166 ACGATGAGTT AG 1272

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167
168 (2) INFORMATION FOR SEQ ID NO:3:
169 (i) SEQUENCE CHARACTERISTICS:
170 (A) LENGTH: 70
171 (B) TYPE: Amino acid
172 (C) TOPOLOGY: Linear
173 (ii) MOLECULE TYPE: Peptide
174 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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175
176 Val Cys His Val Ile Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser
177 1 5 10 15
178 Leu Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met Ile Thr Leu Leu
179 20 25 30
180 Asn Thr Pro Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe
181 35 40 45
182 Gly Lys Gly Met Cys His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu
183 50 55 60
184 His Val Ser Ala Leu Thr
185 65 70
186

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187 (2) INFORMATION FOR SEQ ID NO:4:
188 (i) SEQUENCE CHARACTERISTICS:
189 (A) LENGTH: 71
190 (B) TYPE: Amino acid
191 (C) TOPOLOGY: Linear
192 (ii) MOLECULE TYPE: Peptide
193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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194
195 Glu Pro Ala Asp Leu Phe Trp Lys Asn Leu Asp Leu Pro Thr Phe Ile
196 1 5 10 15
197 Leu Leu Asn Ile Leu Pro Leu Leu Ile Ile Ser Val Ala Tyr Val Arg
198 20 25 30
199 Val Thr Lys Lys Leu Trp Leu Cys Asn Met Ile Val Asp Val Thr Thr
200 35 40 45
201 Glu Gln Tyr Phe Ala Leu Arg Pro Lys Lys Lys Lys Thr Ile Lys Met
202 50 55 60
203 Leu Met Leu Val Val Val Leu
204 65 70
205

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RAW SEQUENCE LISTING
PATENT APPLICATION US/10/067,477DATE: 05/02/2002
TIME: 15:07:21

INPUT SET: S36844.raw

206 (2) INFORMATION FOR SEQ ID NO:5:
207 (i) SEQUENCE CHARACTERISTICS:
208 (A) LENGTH: 210
209 (B) TYPE: Nucleic acid
210 (C) STRANDEDNESS: Double
211 (C) TOPOLOGY: Linear
212 (ii) MOLECULE TYPE: cDNA
213 (xi) FEATURE:
214 (C) IDENTIFICATION METHOD: S
215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
216
217 GTCTGTTCATG TCATCTTCAA GAACCAGCGA ATGCACTCGG CCACCAGCCT CTTTCATCGTC 60
218 AACCTGGCAG TTGCCGACAT AATGATCAG CTGCTCAACA CCCCTTCAC TTTGGTTCGC 120
219 TTTGTGAACA GCACATGGAT ATTTGGGAAG GGCATGTGCC ATGTCAGCCG CTTTGCCAG 180
220 TACTGCTCAC TGCACGTCTC AGCACTGACA 210
221
222 (2) INFORMATION FOR SEQ ID NO:6:
223 (i) SEQUENCE CHARACTERISTICS:
224 (A) LENGTH: 213
225 (B) TYPE: Nucleic acid
226 (C) STRANDEDNESS: Double
227 (C) TOPOLOGY: Linear
228 (ii) MOLECULE TYPE: cDNA
229 (xi) FEATURE:
230 (C) IDENTIFICATION METHOD: S
231 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
232
233 GAGCCAGCTG ACCTCTTCTG GAAGAACCTG GACTTGCCCA CCTTCATCCT GCTCAACATC 60
234 CTGCCCCCTC TCATCATCTC TGTGGCCTAC GTTCGTGTGA CCAAGAACT GTGGCTGTGT 120
235 AATATGATTG TCGATGTGAC CACAGAGCAG TACTTTGCCC TCGGCCCCAA AAAGAAGAAG 180
236 ACCATCAAGA TGTTGATGCT GGTGGTAGTC CTC 213
237
238 (2) INFORMATION FOR SEQ ID NO:7:
239 (i) SEQUENCE CHARACTERISTICS:
240 (A) LENGTH: 25
241 (B) TYPE: Nucleic acid
242 (C) STRANDEDNESS: Single
243 (C) TOPOLOGY: Linear
244 (ii) MOLECULE TYPE: Other nucleic acid Synthetic
245 DNA
246 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
247
248 CGTGGSCMTS STGGGCAACN YCCTG 25
249
250 (2) INFORMATION FOR SEQ ID NO:8:
251 (i) SEQUENCE CHARACTERISTICS:
252 (A) LENGTH: 27
253 (B) TYPE: Nucleic acid
254 (C) STRANDEDNESS: Single
255 (C) TOPOLOGY: Linear
256 (ii) MOLECULE TYPE: Other nucleic acid Synthetic
257 DNA
258 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/10/067,477DATE: 05/02/2002
TIME: 15:07:21**INPUT SET: S36844.raw**

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Shuji HINUMA
7	Unknown or Misplaced Identifier	(B) STREET: 7-9-1402, Kasuga 1-chome
8	Unknown or Misplaced Identifier	(C) CITY: Tsukuba
9	Unknown or Misplaced Identifier	(D) STATE: Ibaraki
10	Unknown or Misplaced Identifier	(E) COUNTRY: Japan
11	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 305
14	Unknown or Misplaced Identifier	(A) NAME: Junichi SAKAMOTO
15	Unknown or Misplaced Identifier	(B) STREET: 14-30-A103, Kamishinden 1-chome
16	Unknown or Misplaced Identifier	(C) CITY: Toyonaka
17	Unknown or Misplaced Identifier	(D) STATE: Osaka
18	Unknown or Misplaced Identifier	(E) COUNTRY: Japan
19	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 565
22	Unknown or Misplaced Identifier	(A) NAME: Masaki HOSOYA
23	Unknown or Misplaced Identifier	(B) STREET: 711-83, Itaya 1-chome
24	Unknown or Misplaced Identifier	(C) CITY: Tsuchiura
25	Unknown or Misplaced Identifier	(D) STATE: Ibaraki
26	Unknown or Misplaced Identifier	(E) COUNTRY: Japan
27	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 300

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/10/067,477

DATE: 05/02/2002
TIME: 15:07:21

INPUT SET: S36844.raw

GENERAL INFORMATION

More Identifiers Found Than MAX Allowed

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/10/067,477DATE: 05/02/2002
TIME: 15:07:21**INPUT SET: S36844.raw**

Line	Original Text	Corrected Text
51	(C) CLASSIFICATION	(C) CLASSIFICATION:
138	(C) STRANDENESS: Double	(C) STRANDEDNESS: Double
141	(xi) FEATURE	(xi) FEATURE:
210	(C) STRANDENESS: Double	(C) STRANDEDNESS: Double
213	(xi) FEATURE	(xi) FEATURE:
226	(C) STRANDENESS: Double	(C) STRANDEDNESS: Double
229	(xi) FEATURE	(xi) FEATURE: